

0570  
1026

#2

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/970,624

DATE: 10/17/2001  
 TIME: 10:31:38

Input Set : A:\1263.SEQLIST.TXT  
 Output Set: N:\CRF3\10172001\I970624.raw

ENTERED

4 <110> APPLICANT: Bruce, Wesley B.  
 6 <120> TITLE OF INVENTION: A Nitrate-Responsive Root  
 7 Transcriptional Factor  
 9 <130> FILE REFERENCE: 1263  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/970,624  
 C--> 11 <141> CURRENT FILING DATE: 2001-10-04  
 11 <150> PRIOR APPLICATION NUMBER: US 60/238,292  
 12 <151> PRIOR FILING DATE: 2000-10-05  
 14 <160> NUMBER OF SEQ ID NOS: 2  
 16 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 1280  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: Zea mays  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: CDS  
 25 <222> LOCATION: (360)...(1082)  
 27 <400> SEQUENCE: 1  
 28 gcacgagccg cctgcgcc agaaaagcca tcgttcttcc cacaaacgca cacatagaag 60  
 29 catcattccc ctctcggcta gcttcttccct ctctctccct cctcctcctc ttctcttctc 120  
 30 tcttcccttg ggaacctgc tgcctttgag ctttcttctt cgagagctcc caccagatct 180  
 31 cctcctcctt accttctttg gcacgttcgg cggcgcgcg cgagaaagat agatcccggc 240  
 32 atcgctcgtc tgcgtccttg cttccgatcg gagggccaca accacaacct ctcgctccat 300  
 33 agcgtgcaag cgcgagccag ggtcaagaag agagctagct agctataggc cggagatcg 359  
 34 atg ggg agg gga aag atc gtg atc cgc agg atc gat aac tcc acg agc 407  
 35 Met Gly Arg Gly Lys Ile Val Ile Arg Arg Ile Asp Asn Ser Thr Ser  
 36 1 5 10 15  
 38 cgg cag gtg acc ttc tcc aag cgc cgg aac ggg atc ttc aag aag gcc 455  
 39 Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala  
 40 20 25 30  
 42 aag gag ctc gcc atc ctc tgc gat gcg gag gtc ggc ctc gtc atc ttc 503  
 43 Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Val Ile Phe  
 44 35 40 45  
 46 tcc agc acc ggc cgc ctc tac gag tac tct agc acc agc atg aaa tca 551  
 47 Ser Ser Thr Gly Arg Leu Tyr Glu Tyr Ser Ser Thr Ser Met Lys Ser  
 48 50 55 60  
 50 gtt ata gat cgg tac ggc aag gcc aag gaa gag cag caa gtc gtc gca 599  
 51 Val Ile Asp Arg Tyr Gly Lys Ala Lys Glu Glu Gln Gln Val Val Ala  
 52 65 70 75 80  
 54 aat ccc aac tcg gag ctt aag ttt tgg caa agg gag gca gca agc ttg 647  
 55 Asn Pro Asn Ser Glu Leu Lys Phe Trp Gln Arg Glu Ala Ala Ser Leu  
 56 85 90 95  
 58 aga caa caa ctg cac aac ttg caa gaa aat tat cgg cag ttg acg gga 695  
 59 Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly  
 60 100 105 110  
 62 gat gat ctt tct ggg ctg aat gtc aaa gaa ctg cag tcc ctg gag aat 743  
 63 Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser Leu Glu Asn

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64          115          120          125
66  caa ttg gaa aca agc ctg cgt ggt gtc cgc gca aag aag gac cat ctc      791
67  Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala Lys Lys Asp His Leu
68          130          135          140
70  ttg ata gat gag att cac gat ttg aat cga aag gca agt tta ttt cac      839
71  Leu Ile Asp Glu Ile His Asp Leu Asn Arg Lys Ala Ser Leu Phe His
72  145          150          155          160
74  caa gaa aat aca gac ttg tac aat aag atc aac ctg att cgc caa gaa      887
75  Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn Leu Ile Arg Gln Glu
76          165          170          175
78  aat gat gag tta cat aaa aag ata tat gag act gaa gga cca agt gga      935
79  Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr Glu Gly Pro Ser Gly
80          180          185          190
82  gtt aat cgg gag tca ccg act cca ttc aac ttt gca gta gta gaa acc      983
83  Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe Ala Val Val Glu Thr
84          195          200          205
86  aga gat gtt cct gtg caa ctt gaa ctc agc aca ctg cca cag caa aat      1031
87  Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr Leu Pro Gln Gln Asn
88          210          215          220
90  aac att gag cca tct act gct cct aag cta gga ttg caa tta att cca      1079
91  Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly Leu Gln Leu Ile Pro
92  225          230          235          240
94  tga agaagagtaa aactgccgtc ttatgatgct gaaggaaact atttattgtg      1132
95  *
W--> 98  aagagatgat actcagagaa agacatatatt gtggcagggg gatttgagat atgaacttat      1192
99  aaatgtaatg caaataattt tcagaccgga atggggtcgt ggaattcaga ggatgattgc      1252
100  tttctaaaaa aaaaaaaaaa aaaaaaaa      1280
102 <210> SEQ ID NO: 2
103 <211> LENGTH: 240
104 <212> TYPE: PRT
105 <213> ORGANISM: Zea mays
107 <400> SEQUENCE: 2
108  Met Gly Arg Gly Lys Ile Val Ile Arg Arg Ile Asp Asn Ser Thr Ser
109  1          5          10          15
110  Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala
111          20          25          30
112  Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Val Ile Phe
113          35          40          45
114  Ser Ser Thr Gly Arg Leu Tyr Glu Tyr Ser Ser Thr Ser Met Lys Ser
115          50          55          60
116  Val Ile Asp Arg Tyr Gly Lys Ala Lys Glu Glu Gln Gln Val Val Ala
117  65          70          75          80
118  Asn Pro Asn Ser Glu Leu Lys Phe Trp Gln Arg Glu Ala Ala Ser Leu
119          85          90          95
120  Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly
121          100          105          110
122  Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser Leu Glu Asn
123          115          120          125
124  Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala Lys Lys Asp His Leu

```

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125	130	135	140													
126	Leu	Ile	Asp	Glu	Ile	His	Asp	Leu	Asn	Arg	Lys	Ala	Ser	Leu	Phe	His
127	145				150						155				160	
128	Gln	Glu	Asn	Thr	Asp	Leu	Tyr	Asn	Lys	Ile	Asn	Leu	Ile	Arg	Gln	Glu
129					165						170				175	
130	Asn	Asp	Glu	Leu	His	Lys	Lys	Ile	Tyr	Glu	Thr	Glu	Gly	Pro	Ser	Gly
131				180					185					190		
132	Val	Asn	Arg	Glu	Ser	Pro	Thr	Pro	Phe	Asn	Phe	Ala	Val	Val	Glu	Thr
133			195					200					205			
134	Arg	Asp	Val	Pro	Val	Gln	Leu	Glu	Leu	Ser	Thr	Leu	Pro	Gln	Gln	Asn
135		210				215					220					
136	Asn	Ile	Glu	Pro	Ser	Thr	Ala	Pro	Lys	Leu	Gly	Leu	Gln	Leu	Ile	Pro
137	225					230					235				240	

## VERIFICATION SUMMARY

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Input Set : A:\1263.SEQLIST.TXT

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1